

AMENDMENTS IN THE SPECIFICATION

Please amend the paragraph beginning at page 7, line 27 as follows:

The sucrose phosphorylase having improved thermostability of the present invention is a sucrose phosphorylase having improved thermostability, obtained by modifying a natural sucrose phosphorylase,

wherein the sucrose phosphorylase having improved thermostability has an amino acid residue which is different from that of the natural sucrose phosphorylase, in at least one position selected from the group consisting of:

a position corresponding to position 14, a position corresponding to position 29 and a position corresponding to position 44 in motif sequence 1:

AVGGVHLLPFFPSTGDRGFAPIDYHEVDSAFGDWDDVKRLGEKYYLMFDFMINHIS
(SEQ ID NO. 25);

a position corresponding to position 7, a position corresponding to position 19, a position corresponding to position 23 and a position corresponding to position 34 in motif sequence 2:

RPTQEDVDLIYKRKDRAPKQEIQFADGSVEHLWNTFGEEQID (SEQ ID NO. 26); and
a position corresponding to position 19 in motif sequence 3:

ILPEIHEHYTIQFKIADHDYVYDFALPMVTLYSLYSG (SEQ ID NO. 27); and

wherein the enzyme activity of the sucrose phosphorylase having improved thermostability at 37°C, after heating the sucrose phosphorylase having improved thermostability in 20 mM Tris buffer (pH 7.0) at 55°C for 20 minutes, is 20% or more of the enzyme activity of the sucrose phosphorylase having improved thermostability at 37°C before heating.

Please amend the paragraph beginning at page 12, line 30 as follows:

One method of the present invention is a method for producing a sucrose phosphorylase having improved thermostability comprising:

modifying a first nucleic acid molecule comprising a base sequence encoding a first sucrose phosphorylase to obtain a second nucleic acid molecule comprising a modified base sequence;

preparing an expression vector comprising the second nucleic acid molecule; introducing the expression vector into a cell to express a sucrose phosphorylase having improved thermostability; and

recovering the expressed sucrose phosphorylase having improved thermostability,

wherein the sucrose phosphorylase having improved thermostability has an amino acid residue which is different from the amino acid residue of the first sucrose phosphorylase in at least one position selected from the group consisting of:

a position corresponding to position 14, a position corresponding to position 29 and a position corresponding to position 44 in motif sequence 1:

AVGGVHLLPFFPSTGDRGFAPIDYHEVDSAFGDWDDVKRLGEKYYLMFDFMINHIS
(SEQ ID NO. 25);

a position corresponding to position 7, a position corresponding to position 19, a position corresponding to position 23 and a position corresponding to position 34 in motif sequence 2:

RPTQEDVDLIYKRKDRAPKQEIQFADGSVEHLWNTFGEEQID (SEQ ID NO. 26); and

a position corresponding to position 19 in motif sequence 3:
ILPEIHEHYTIQFKIADHDYVYDFALPMVTLYSLYSG (SEQ ID NO. 27); and

wherein the enzyme activity of the sucrose phosphorylase having improved thermostability at 37°C, after heating the sucrose phosphorylase having improved thermostability in 20 mM Tris buffer (pH 7.0) at 55°C for 20 minutes, is 20% or more of the enzyme activity of the sucrose phosphorylase having improved thermostability at 37°C before heating.

Please amend the BRIEF DESCRIPTION OF THE DRAWINGS beginning on page 28, line 30 as follows:

Fig. 1A: Fig. 1A is a view showing amino acid sequences of sucrose phosphorylases derived from some organisms, which are aligned in multiple alignment by GENETYX-WIN Ver. 4.0. The sucrose phosphorylases are StMuSP (SEQ ID NO. 2); StPSP (SEQ ID NO. 4); StSSP (SEQ ID NO. 6); StMiSP (SEQ ID NO. 12); LeuSP1 (SEQ ID NO. 8); LeuSP2 (SEQ ID NO. 14); OenSP (SEQ ID NO. 10); LBSP1 (SEQ ID NO. 16); LBSP2 (SEQ ID NO. 18); and ListSP (SEQ ID NO. 20). Fig. 1A is followed by Fig. 1B.

Please amend the paragraph beginning at page 67, line 6 as follows:

In this manner, the position of an amino acid residue which improves thermostability can be also specified using the motif sequences. A position of an amino acid residue which improves thermostability can be at least one position selected from the group consisting of a position corresponding to position 14, a position corresponding to position 29 and a position corresponding to position 44 in motif sequence 1:

AVGGVHLLPFFPSTGDRGFAPIDYHEVDSAFGDWDDVKRLGEKYYLMFDFMINHIS (SEQ ID NO. 25); a position corresponding to position 7, a position corresponding to position 19, a position corresponding to position 23 and a position corresponding to position 34 in motif sequence 2:

RPTQEDVDLIYKRKDRAPKQEIQFADGSVEHLWNTFGEEQID (SEQ ID NO. 26); and a position corresponding to position 19 in motif sequence 3:
ILPEIHEHYTIQFKIADHDYVYDFALPMVTLYSLYS (SEQ ID NO. 27).

Please amend the paragraph beginning at page 67, line 23 as follows:

Therefore, in the method according to the present invention, it can be said that a nucleic acid molecule comprising a base sequence encoding first sucrose phosphorylase is modified so that the sucrose phosphorylase having improved thermostability, encoded by a modified nucleic acid has an amino acid residue which is different from an amino acid residue of the natural sucrose phosphorylase in at least one position selected from the group consisting of a position corresponding to position 14, a position corresponding to position 29 and a position corresponding to position 44 in motif sequence 1:

AVGGVHLLPFFPSTGDRGFAPIDYHEVDSAFGDWDDVKRLGEKYYLMFDFMINHIS
(SEQ ID NO. 25); a position corresponding to position 7, a position corresponding to position 19, a position corresponding to position 23 and a position corresponding to position 34 in motif sequence 2:

RPTQEDVDLIYKRKDRAPKQEIQFADGSVEHLWNTFGEEQID (SEQ ID NO. 26); and a position corresponding to position 19 in motif sequence 3:

ILPEIHEHYTIQFKIADHDYVYDFALPMVTLYSLYS (SEQ ID NO. 27).

Please amend the paragraph beginning at page 69, line 3 as follows:

As used herein, "a position corresponding to position 14 in a motif sequence 1: AVGGVHLLPFFPSTGDRGFAPIDYHEVDSAFGDWDDVKRLGEKYYLMFDFMINHIS" (SEQ ID NO. 25) refers to position which is aligned with amino acid residue at position 14 in motif sequence 1 when a subject amino acid sequence and motif sequence 1 are aligned, without inserting a gap, so that homology between sequences is greatest. More preferably, it refers to the position which is aligned with the amino acid residue at position 14 in motif sequence 1 when the amino acid sequence of motif sequence 1 and a subject amino acid sequence are aligned under the condition of GAP Penalty (Peptide): Insert=-8, Extend=-3, gap Extend on top position: setted (checked), Match

Mode: Local Match using a score table of default, in multiple alignment of
GENETYX-WIN Ver.4.0.